DESCRIPTION

METHOD OF DIAGNOSING RISK OF MYOCARDIAL INFARCTION

TECHNICAL FIELD

The present invention relates to a detection method using genes associated with myocardial infarction. More particularly, it relates to a detection method using a plurality of gene polymorphisms associated with myocardial infarction and to a kit used for the method. The present invention can be used for, for example, diagnosing a risk of myocardial infarction.

BACKGROUND ART

Myocardial infarction is a multifactorial disease and its development is defined by the interaction between individual's genetic background and various environmental factors (Marenberg ME, Risch N, Berkman LF, Floderus B, de Faire U. Genetic susceptibility to death from coronary heart disease in a study of twins. N Engl J Med 1994;330:1041-1046., Nora JJ, Lortscher RH, Spangler RD, Nora AH, Kimberling WJ. Genetic-epidemiologic study of early-onset ischemic heart disease. Circulation 1980;61: 503-508). In general, the risk of myocardial infarction is increased in proportion to the number of conventional risk factors such as hypertension, diabetes, hyperlipidemia, etc (Nora JJ, Lortscher RH, Spangler RD, Nora AH, Kimberling WJ. Genetic-epidemiologic study of early-onset ischemic heart disease. Circulation 1980; 61: 503-508). These risk factors themselves are partially regulated by genetic factors. However, since a family history is an independent predictable factor of myocardial infarction, it is suggested that there are genetic

factors susceptible for myocardial infarction other than conventional risk factors (Marenberg ME, Risch N, Berkman LF, Floderus B, de Faire U. Genetic susceptibility to death from coronary heart disease in a study of twins. N Engl J Med 1994; 330: 1041-1046). In addition, cases in which myocardial infarction may be developed without any conventional risk factors also suggest the relationship between myocardial infarction and genetic factors.

Myocardial infarction is a disease with the highest mortality in the Western countries. Even in the case where myocardial infarction is not lethal, it may be complicated with heart failure, angina pectoris and refractory arrhythmia, thus deteriorating the quality of life of patients. Therefore, needless to say, it is important to prevent myocardial infarction. One of the methods for preventing myocardial infarction is to identify genes susceptible for myocardial infarction. By linkage analysis (Broeckel U, Hengstenberg C, Mayer B, et al. A comprehensive linkage analysis for myocardial infarction and its related risk factors. Nature genet 2002;30:210-214) and association studies by candidate genes (Cambien F, Poirier O, Lecerf L, et al. Deletion polymorphism in the gene for angiotensin-converting enzyme is a potent risk factor for myocardial infarction. Nature 1992; 359: 641-644. Weiss EJ, Bray PF, Tayback M, et al. A polymorphism of a platelet glycoprotein receptor as an inherited risk factor for coronary thrombosis. N Engl J Med 1996; 334: 1090-1094., Iacoviello L, Di Castelnuovo A, De Knijff P, et al. Polymorphisms in the coagulation factor VII gene and the risk of myocardial infarction. N Engl J Med 1998;338:79-85., Kuivenhoven JA, Jukema JW, Zwinderman AH, et al. The role of a common variant of the

cholesterol ester transfer protein gene in the progression of coronary atherosclerosis. N Engl J Med 1998; 338: 86-93), gene locus on the chromosome and some candidate genes which are associated with myocardial infarction have been identified. Previously, by studies of genetic epidemiology, there have been reported the relationships between the myocardial infarction and gene polymorphisms such as angiotensin converting enzyme (Cambien F, Poirier O, Lecerf L, et al. Deletion polymorphism in the gene for angiotensin-converting enzyme is a potent risk factor for myocardial infarction. Nature 1992; 359: 641-644), platlet glycoprotein IIIa (Weiss EJ, Bray PF, Tayback M, et al. A genetical polymorphism of a platelet glycoprotein receptor as an inherited risk factor for coronary thrombosis. N Engl J Med 1996; 334: 1090-1094), blood coagulation factor VII, cholesterol ester tnrasfer protein (Kuivenhoven JA, Jukema JW, Zwinderman AH, et al. The role of a common variant of the cholesterol ester transfer protein gene in the progression of coronary atherosclerosis. N Engl J Med 1998; 338: 86-93), and the like. However, there have been conflicting reports, certain conclusion has never been reached. Furthermore, since different races have different gene polymorphisms, it is important to construct a database as to the relationship between polymorphisms and myocardial infarction in each race.

DISCLOSURE OF INVENTION

As mentioned above, a large number of relation analyses between gene polymorphisms and coronary artery disease or myocardial infarction have been carried out previously. However, many studies have not reached a certain finding in terms of significance thereof. This is mainly because populations of

subjects in many studies are not sufficient and not only gene polymorphisms but also environmental factors are different between races. Furthermore, even if the relationship with myocardial infarction is recognized, in the analysis of large scale population, relative risk (odds ratio) is generally low.

The present invention was made on the basis of the above-mentioned background, and the object thereof is to provide a means of diagnosing genetic risk of myocardial infarction with high accuracy and high predictability and to contribute to a primary prevention of myocardial infarction.

To achieve the above-mentioned objects, the present inventors have extracted 71 genes which were estimated to be associated with coronary arteriosclerosis, coronary artery spasm, hypertension, diabetes, hyperlipidemia, etc., and mainly selected 112 polymorphisms which were predicted to be associated with functional changes of genes by the use of a plurality of public databases. Then, as to 112 polymorphisms of 71 genes, a large scale relation analysis of more than 5000 cases was carried out. As a result, the present inventors succeeded in identifying ten SNPs (single nucleotide polymorphisms) which were associated with myocardial infarction in males and five SNPs in females. In addition, by using the combination of these polymorphisms, it was found that in a stepwise forward selection of multivariate logistic regression analysis, a maximum odds ratio of 11.26 in males and maximum odds ratio of 88.51 in females were presented. Based on these results, it was possible to obtain a finding in that by selecting a plurality of SNPs from these SNPs and using the combination of the results of analysis of each SNP, diagnosis of myocardial infarction can be carried out with high reliability and high predictability. Meanwhile as to one of the five SNPs

that were found to be associated with myocardial infarction in females, even by analyzing the polymorphism singly, extremely high odds ratio could be obtained. The present invention was completed based on the above findings and provides the following configuration.

[1] A method for detecting the genotype in a nucleic acid sample, comprising the following step (a):

(a) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (10) in a nucleic acid sample:

(1) polymorphism at the base number position 1019 of the connexin 37 gene;

(2) polymorphism at the base number position -863 of the tumor necrosis factor α gene;

(3) polymorphism at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) polymorphism at the base number position -6 of the angiotensinogen gene:

(5) polymorphism at the base number position -219 of the apolipoprotein E gene;

(6) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(8) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(9) polymorphism at the base number position -819 of the interleukin-10 gene; and

(10) polymorphism at the base number position -592 of the

interleukin-10 gene.

[2] A method for detecting the genotype in a nucleic acid sample, comprising the following step (b):

(b) analyzing two or more polymorphisms selected from the group consisting of the following (11) to (15) in a nucleic acid sample:

(11) polymorphism at the base number position -1171 of the stromelysin 1 gene;

(12) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) polymorphism at the base number position 1018 of the glycoprotein Ibα gene;

(14) polymorphism at the base number position 584 of the paraoxonase gene: and

(15) polymorphism at the base number position 4070 of the apolipoprotein E gene.

[3] A method for detecting the genotype in a nucleic acid sample, comprising the following step (c):

(c) analyzing polymorphism at the base number position 4070 of the apolipoprotein E gene in a nucleic acid sample.

[4] A method for diagnosing the risk of myocardial infarction, comprising the following steps (i) to (iii):

(i) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (10) in a nucleic acid sample:

(1) polymorphism at the base number position 1019 of the connexin 37 gene;

(2) polymorphism at the base number position -863 of the tumor necrosis factor α gene;

(3) polymorphism at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) polymorphism at the base number position -6 of the angiotensinogen gene:

(5) polymorphism at the base number position -219 of the apolipoprotein E gene;

(6) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(8) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(9) polymorphism at the base number position -819 of the interleukin-10 gene; and

(10) polymorphism at the base number position -592 of the interleukin-10 gene;

(ii) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(iii) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

[5] A method for diagnosing the risk of myocardial infarction, comprising the following steps (iv) to (vi):

(iv) analyzing two or more polymorphisms selected from the group consisting of the following (11) to (15) in a nucleic acid sample:

(11) polymorphism at the base number position -1171 of

the stromelysin 1 gene;

(12) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) polymorphism at the base number position 1018 of the glycoprotein Ibα gene;

(14) polymorphism at the base number position 584 of the paraoxonase gene: and

(15) polymorphism at the base number position 4070 of the apolipoprotein E gene;

(v) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(vi) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

[6] A method for diagnosing the risk of myocardial infarction, comprising the following steps (vii) to (ix):

(vii) analyzing polymorphism at the base number position 4070 of the apolipoprotein E gene in a nucleic acid sample;

(viii) determining, based on the information about polymorphism which was obtained in the step (vii), the genotype of the nucleic acid sample; and

(ix) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

[7] A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (1) to (10):

(1) a nucleic acid for polymorphism analysis at the base number position 1019 of the connexin 37 gene;

(2) a nucleic acid for polymorphism analysis at the base number position -863 of the tumor necrosis factor α gene;

(3) a nucleic acid for polymorphism analysis at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) a nucleic acid for polymorphism analysis at the base number position -6 of the angiotensinogen gene:

(5) a nucleic acid for polymorphism analysis at the base number position -219 of the apolipoprotein E gene;

(6) a nucleic acid for polymorphism analysis at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) a nucleic acid for polymorphism analysis at the base number position -482 of the apolipoprotein C-III gene;

(8) a nucleic acid for polymorphism analysis at the base number position 1186 of the thrombospondin 4 gene;

(9) a nucleic acid for polymorphism analysis at the base number position -819 of the interleukin-10 gene; and

(10) a nucleic acid for polymorphism analysis at the base number position -592 of the interleukin-10 gene.

[8] A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (11) to (15):

(11) a nucleic acid for polymorphism analysis at the base number position -1171 of the stromelysin 1 gene;

(12) a nucleic acid for polymorphism analysis at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) a nucleic acid for polymorphism analysis at the base number position 1018 of the glycoprotein Ibα gene;

(14) a nucleic acid for polymorphism analysis at the base

number position 584 of the paraoxonase gene: and

(15) a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene.

[9] A kit for detecting the genotype, comprising a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene.

[10] Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (1) to (10) fixed to an insoluble support:

(1) a nucleic acid for polymorphism analysis at the base number position 1019 of the connexin 37 gene;

(2) a nucleic acid for polymorphism analysis at the base number position -863 of the tumor necrosis factor α gene;

(3) a nucleic acid for polymorphism analysis at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) a nucleic acid for polymorphism analysis at the base number position -6 of the angiotensinogen gene:

(5) a nucleic acid for polymorphism analysis at the base number position -219 of the apolipoprotein E gene;

(6) a nucleic acid for polymorphism analysis at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) a nucleic acid for polymorphism analysis at the base number position -482 of the apolipoprotein C-III gene;

(8) a nucleic acid for polymorphism analysis at the base number position 1186 of the thrombospondin 4 gene;

(9) a nucleic acid for polymorphism analysis at the base number position -819 of the interleukin-10 gene; and

(10) a nucleic acid for polymorphism analysis at the base number position -592 of the interleukin-10 gene.

[11] Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (11) to (15) fixed to an insoluble support:

(11) a nucleic acid for polymorphism analysis at the base number position -1171 of the stromelysin 1 gene;

(12) a nucleic acid for polymorphism analysis at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) a nucleic acid for polymorphism analysis at the base number position 1018 of the glycoprotein Ibα gene;

(14) a nucleic acid for polymorphism analysis at the base number position 584 of the paraoxonase gene: and

(15) a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene.

[12] Fixed nucleic acids comprising a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene fixed to an insoluble support.

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 is a table summarizing 112 gene polymorphisms examined in a screening related analysis in Examples.

Fig. 2 is also a table summarizing 112 gene polymorphisms examined in a screening related analysis in Examples.

Fig. 3 is a table summarizing primers (SEQ ID NOs: 30, 31, 32, 21, 22, 23, 15, 16, 17, 24, 25, 26, 18, 19, 20, 33, 34, 35, 42, 43 and 44 in this order from the top), probes (SEQ ID NOs: 59 and 60 in this order from the top) and other conditions used

in order to determine the genotype in Examples. In Fig. 3, FITC denotes fluorescein isothiocyanate and TxR denotes Texas Red, respectively.

Fig. 4 is also a table summarizing primers (SEQ ID NOs: 27, 28, 29, 39, 40, 41, 36, 37, 38, 53, 54, 55, 56, 57, 58, 48, 49, 45, 46, 47, 50, 51 and 52 in this order from the top), probes (SEQ ID NOs: 61, 62, 63 and 64 in this order from the top) and other conditions used in order to determine the genotype in Examples. In Fig. 4, FITC denotes fluorescein isothiocyanate and TxR denotes Texas Red, respectively.

Fig. 5 is a table summarizing the backgrounds of 909 gene polymorphisms examined in a screening related analysis in Examples. Data of age and body mass index are represented by average ± standard deviation. In table, *1 denotes P=0.0278 and *2 denotes P<0.0001 versus controls, respectively.

Fig. 6 is a table summarizing gene polymorphisms which were found to be associated with myocardial infarction.

Fig. 7 is a table summarizing the backgrounds of all 5061 subjects in the relation analysis in Examples. Data of age and body mass index are represented by average ± standard deviation. In table, *1 denotes P=0.022, *2 denotes P<0.001 and *3 denotes P=0.017, respectively.

Fig. 8 is a table summarizing distribution of gene polymorphisms which were found to be associated with myocardial infarction in all 5061 subjects in the relation analysis in Examples.

Fig. 9 is a table showing results of multivariate logistic regression analysis of gene polymorphisms and myocardial infarction in all 5061 subjects in the relation analysis according to Examples. In table, OR denotes odds ratio and CI denotes

confidence interval.

Fig. 10 is a table showing results of stepwise forward selection method of multivariate logistic regression analysis of gene polymorphisms associated with myocardial infarction. In this table, CI denotes confidence interval.

Fig. 11 is a table showing results of diagnosis of genetic risk (risk of development) of myocardial infarction using a combination of 5 gene polymorphisms in male.

Fig. 12 is a table showing results of diagnosis of genetic risk (risk of development) of myocardial infarction using a combination of 5 gene polymorphisms in female.

Fig. 13 is a graph showing the relationship between the number of gene polymorphisms combined and the odds ratio in contracting myocardial infarction. Note here that (A) shows the case of male subjects and (B) shows the case of female subjects.

BEST MODE FOR CARRYING OUT THE INVENTION

The first aspect of the present invention relates to a method for detecting the genotype in a nucleic acid sample. One embodiment of the present invention is featured by including the step of analyzing two or more polymorphisms selected from the group consisting of the following (1) to (10). Furthermore, another embodiment of the present invention is featured by including the step of analyzing two or more polymorphisms selected from the group consisting of the following (11) to (15). In addition, further embodiment of the present invention is featured by including at least the step of analyzing the following (15). Note here that it is possible to determine, based on the information about polymorphism which was obtained in the above-mentioned step, the genotype of the nucleic acid sample; and thereby to assess, based

on the genotype determined, a genetic risk of myocardial infarction.

(1) polymorphism at the base number position 1019 of the connexin 37 gene: 1019C→T (hereinafter, also referred to as "connexin 37 (1019C→T) polymorphism")

(2) polymorphism at the base number position -863 of the tumor necrosis factor α gene: -863C→A (hereinafter, also referred to as "TNFα (-863C→A) polymorphism")

(3) polymorphism at the base number position 242 of the NADH/NADPH oxidase p22 phox gene: 242C→T (hereinafter, also referred to as "NADH/NADPH oxidase p22 phox (242C→T) polymorphism")

(4) polymorphism at the base number position -6 of the angiotensinogen gene: -6G→A (hereinafter, also referred to as "polymorphism angiotensinogen (-6G→A)")

(5) polymorphism at the base number position -219 of the apolipoprotein E gene: -219G→T (hereinafter, also referred to as "Apo E-219 (-219G→T) polymorphism")

(6) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene: 994G→T (hereinafter, also referred to as "PAF acetylhydrolase (994G→T) polymorphism")

(7) polymorphism at the base number position -482 of the apolipoprotein C-III gene: -482C→T (hereinafter, also referred to as "Apo C-III (-482C→T) polymorphism")

(8) polymorphism at the base number position 1186 of the thrombospondin 4 gene: 1186G→C (hereinafter, also referred to as "TSP4 (1186G→C) polymorphism")

(9) polymorphism at the base number position -819 of the interleukin-10 gene: -819T→C (hereinafter, also referred to as "IL-10 (-819T→C) polymorphism")

(10) polymorphism at the base number position -592 of the

Interleukin-10 gene: -592A→C (hereinafter, also referred to as "IL-10 (-592A→C) polymorphism")

(11) polymorphism at the base number position -1171 of the stromelysin 1 gene: -1171/5A→6A (hereinafter, also referred to as "stromelysin 1 (-1171/5A→6A) polymorphism")

(12) polymorphism at the base number position -668 of the plasminogen activator inhibitor 1 gene: -668/4G→5G (hereinafter, also referred to as "PAI1 (-668/4G→5G) polymorphism")

(13) polymorphism at the base number position 1018 of the glycoprotein Ibα gene: 1018C→T (hereinafter, also referred to as "glycoprotein Ibα (1018C→T) polymorphism")

(14) polymorphism at the base number position 584 of the paraoxonase gene: 584G→A (hereinafter, also referred to as "paraoxonase (584G→A) polymorphism")

(15) polymorphism at the base number position 4070 of the apolipoprotein E gene: 4070C→T (hereinafter, also referred to as "Apo E (4070C→T) polymorphism")

In the above, description such as 1019C→T means that polymorphism at the relevant base number position consists of two genotypes, bases before and after the arrow. Herein, -1171/5A→6A means a polymorphism consisting of a genotype having five A (adenines) existing successively in the 3' direction from the base number position -1171 and a genotype having six A existing successively in the 3' direction from the base number position -1171. Similarly, -668/4G→5G means a polymorphism consisting of a genotype having four G (guanines) existing successively in the 3' direction from the base number -668 and a gene having five G existing successively in the 3' direction from the base number -668.

The base number of each gene is expressed using as standards the known sequences which are registered in the public database, GenBank (NCBI). Note here that in the base sequence of SEQ ID NO: 1 (Accession No. M96789 : Homo sapiens connexin 37 (GJA4) mRNA, complete cds), the 1019th base corresponds to the base at position 1019 of the connexin 37 gene. Similarly, in the base sequence of SEQ ID NO: 2 (Accession No. L11698 : Homo sapiens tumor necrosis factor alpha gene, promoter region), the 197th base corresponds to the base at position -863 of tumor necrosis factor α gene; in the base sequence of SEQ ID NO: 3 (Accession No. M61107: Homo sapiens cytochrome b light chain (CYBA) gene, exons 3 and 4), the 684th base corresponds to the base at position 242 of NADH/NADPH oxidase p22 phox gene; in the base sequence of SEQ ID NO: 4 (Accession No. X15323 : H. apiens angiotensinogen gene 5' region and exon 1), the 463th base corresponds to the base at position -6 of angiotensinogen gene; in the base sequence of SEQ ID NO: 5 (Accession No. AF055343: Homo sapiens apolipoprotein E (APOE) gene, 5' regulatory region, partial sequence), the 801th base corresponds to the base at position -219 of the apolipoprotein E gene; in the sequence of SEQ ID NO: 6 (Accession No. U20157 : Human platelet-activating factor acetylhydrolase mRNA, complete cds), the 996th base corresponds to the base at position 994 of the platelet-activating factor acetylhydrolase gene; in the sequence of SEQ ID NO: 7 (Accession No. X13367 : Human DNA for apolipoprotein C-III 5'-flank), the 936th base corresponds to the base at position -482 of the apolipoprotein C-III gene; in the sequence of SEQ ID NO: 8 (Accession No. Z19585 : H. sapiens mRNA for thrombospondin-4), the 1186th base corresponds to the base at position 1186 of the thrombospondin 4 gene; in the sequence of SEQ ID NO: 9 (Accession

No. Z30175 : H. sapiens IL-10 gene for interleukin-10 (promoter)), the 455th base corresponds to the base at position -819 and the 682th base corresponds to the base at position -592 of the interleukin-10 gene, respectively; in the sequence of SEQ ID NO: 10 (Accession No. U43511 : Homo sapiens stromelysin-1 gene, promoter region), the 698th base corresponds to the base at position -1171 of the stromelysin 1 gene; in the sequence of SEQ ID NO: 11 (Accession No. X13323 : Human gene for plasminogen activator inhibitor 1 (PAI-1) 5'-flank and exon 1), the 131th base corresponds to the base at position -668 of the plasminogen activator inhibitor 1 gene; in the sequence of SEQ ID NO: 12 (Accession No. J02940 : Human platelet glycoprotein Ib alpha chain mRNA, complete cds), the 524th base corresponds to the base at position 1018 of the glycoprotein Ibα gene; in the sequence of SEQ ID NO: 13 (Accession No. M63012 : H. sapiens serum paraoxonase (PON) 1 mRNA, complete cds), the 584th base corresponds to the base at position 584 of the paraoxonase gene; and in the sequence of SEQ ID NO: 14 (Accession No. M10065 : Human apolipoprotein E (epsilon-4 allele) gene, complete cds), the 4070th base corresponds to the base at position 4070 of the apolipoprotein E gene.

In the present invention, "analyzing polymorphism" refers to the investigation as to what genotype a nucleic acid sample has in the gene polymorphism to be analyzed. It is the same meaning as the investigation on the base (base sequence) of the position in which the polymorphism exists. Typically, for example, in the case of the analysis of the connexin 37 (1019C→T) polymorphism, it refers to investigation on what genotype, i.e., TT (homozygote of allele T) or CT (heterozygote of allele C and allele T) or CC (homozygote of allele C), the connexin 37 gene in a nucleic acid

sample has.

As shown in Examples mentioned below, the polymorphisms mentioned (1) to (10) above are polymorphisms that are recognized as being particularly effective to be used in determining genetic risk of myocardial infarction in an analysis of Japanese male subjects. Therefore, analysis targeting these polymorphisms enables diagnosis with higher accuracy and with higher predictability when subjects are males, particularly, Japanese males.

Similarly, as shown in Examples mentioned below, the polymorphisms mentioned (11) to (15) above are polymorphisms that are recognized as being particularly effective to be used in determining genetic risk of myocardial infarction in an analysis of Japanese female subjects. Therefore, analysis targeting these polymorphisms enables diagnosis with higher accuracy and with higher predictability when subjects are females, particularly, Japanese females. Among these polymorphisms, as to the polymorphism described in (15), as shown in Examples mentioned below, it was confirmed that by analyzing the polymorphism, it was possible to determine the genetic risk of myocardial infarction with extremely high odds ratio. Therefore, by analyzing this polymorphism singly, it is possible to determine the genetic risk of myocardial infarction with high accuracy and high predictability. Of course, in addition to the analysis of the polymorphism (15), analysis of any one or a plurality of polymorphisms selected from (11) to (14) is carried out in combination, and thereby it may be possible to detect the genotype or to diagnose a genetic risk of myocardial infarction.

Herein, in principle, in proportion to the increase in the number of polymorphisms to be analyzed, the genotypes of nucleic acid sample are classified more finely. Thereby, it is possible to diagnose a genetic risk of myocardial infarction with higher predictability. From this viewpoint, it is preferable to detect the genotype by analyzing a larger number of polymorphisms in the above-mentioned polymorphisms (1) to (10). Therefore, it is the most preferable to analyze all of the polymorphisms (1) to (10). In the case where detection is carried out by combining nine or less of polymorphisms, it is possible to preferentially select the polymorphisms with higher odds ratios as in Examples mentioned below. For example, in the case where eight polymorphisms are used in combination, it is preferable to select nine polymorphisms with higher odds ratio, that is, to select (1), (3), (5), (6), (7), (8), (9) and (10). Similarly, in the case where seven polymorphisms are used in combination, it is preferable to select (1), (3), (5), (6), (8), (9) and (10). Similarly, in the case where 6 polymorphisms are used in combination, it is preferable to select (1), (5), (6), (8), (9) and (10). Similarly, in the case where five polymorphisms are used in combination, it is preferable to select (1), (5), (6), (8), and (9).

Similarly, in the case where two or more polymorphisms selected from the group consisting of polymorphisms (11) to (15), it is most preferable to analyze all these polymorphisms, that is, five polymorphisms. In the case where detection is carried out by combining four or less of polymorphisms, it is possible to preferentially select the polymorphisms with higher odds ratios in Examples mentioned below. For example, in the case where four

polymorphisms are used in combination, it is preferable to select four polymorphisms with higher odds ratio, that is, to select (11), (12), (14) and (15). Similarly, in the case where three polymorphisms are used in combination, it is preferable to select (11), (12) and (15). Similarly, in the case where two polymorphisms are used in combination, it is preferable to select (11) and (15).

A method for analyzing each genetic polymorphism is not particularly limited. Known methods may include, for example, amplification by PCR using an allele-specific primer (and probe), a method for polymorphism analysis of amplified product by means of fluorescence or luminescence, PCR-RFLP (polymerase chain reaction-restriction fragment length polymorphism) method, PCR-SSCP (polymerase chain reaction-single strand conformation polymorphism) method (Orita, M. et al., Proc. Natl. Acad. Sci., U.S.A., 86, 2766-2770 (1989), etc.), PCR-SSO (specific sequence oligonucleotide) method, which use PCR method, ASO (allele specific oligonucleotide) hybridization method combining the PCR-SSO method and a dot hybridization method (Saiki, Nature, 324, 163-166 (1986), etc.), or TaqMan-PCR method (Livak, KJ, Genet Anal, 14, 143 (1999), Morris, T. et al., J. Clin. Microbiol., 34, 2933 (1996)), Invader method (Lyamichev V et al., Nat Biotechnol, 17, 292 (1999)), MALDI-TOF/MS (matrix) method using a primer extension method (Haff LA, Smirnov IP, Genome Res 7, 378 (1997)), RCA (rolling cycle amplification) method (Lizardi PM et al., Nat Genet 19, 225 (1998)), a method using DNA microchip or micro-array (Wang DG et al., Science 280, 1077 (1998), etc.)), a primer extension method, a Southern blot hybridization method, a dot hybridization method (Southern, E., J. Mol. Biol. 98, 503-517 (1975)), etc.), or the like. Furthermore, an analysis may be made by direct sequencing of the

portion of polymorphism which is subject to analysis. Note here that polymorphisms may be analyzed by combining these methods ad libitum.

In the case where the amount of nucleic acid sample is small, it is preferable to analyze it by a method using PCR (for example, PCR-RFLP method) from the viewpoint of detection sensitivity or accuracy. Furthermore, any of the above-mentioned analysis methods may be employed after nucleic acid sample is amplified in advance (including a partial region of nucleic acid sample) by a gene amplification such as PCR method or a method applying PCR method.

Meanwhile, in the case where a large number of nucleic acid samples are analyzed, a method capable of analyzing a large number of samples in a relatively short period of time, particularly, for example, allele-specific PCR method, allele-specific hybridization method, TaqMan-PCR method, Invader method, MALDI-TOF/MS (matrix) method using primary extension method, RCA (rolling cycle amplification) method, or a method using a DNA chip or a micro-array.

The above methods use nucleic acids (also called "nucleic acids for polymorphism analysis" in the present invention), e.g., primer and probe in accordance with each method. Example of the nucleic acids for polymorphism analysis may include: a nucleic acid with a sequence complementary to a given region including the site of polymorphism (partial DNA region) in the gene which contains polymorphism that is subject to the analysis; and a nucleic acid (primer) which has a sequence complementary to a given region

including the site of polymorphism(partial DNA region) and which is designed to allow the specific amplification of the DNA fragment containing the relevant site of polymorphism. In the case where polymorphism at position 1019 of the connexin 37 gene is a subject to be analyzed, an example of such nucleic acids includes a nucleic acid having a sequence complementary to a partial DNA region including the position 1019 of the connexin 37 gene in which the base at position 1019 is C (cytosine), or a nucleic acid having a sequence complementary to a partial DNA region including the position 1019 of the connexin 37 gene in which the base at position 1019 is T (thymine).

Other concrete examples of nucleic acids for polymorphism analysis may include a set of nucleic acids which is designed to specifically amplify the partial DNA region that contains the relevant site of polymorphism only in the case where the site of polymorphism that is a subject to the analysis is a certain genotype. A more concrete example may include for example, a set of nucleic acids which is designed to specifically amplify the partial DNA region including the site of polymorphism that is subject to the analysis and which consists of a sense primer that specifically hybridizes the partial DNA region including the relevant site of polymorphism in an antisense strand whose site of polymorphism is a certain genotype and of an antisense primer that specifically hybridizes a partial region of the sense strand. In the case where polymorphism at position 1019 of the connexin 37 gene is a subject to the analysis, examples of such a set of nucleic acids include a set of nucleic acids which is designed to specifically amplify the partial DNA region including the base at position 1019 of the connexin 37 gene and which consists of a sense primer that

specifically hybridizes the partial DNA region containing the base at position 1019 in the antisense strand of the connexin 37 gene whose base at 1019 is C (cytosine) and of an antisense primer that specifically hybridizes a partial region of the sense strand; or a set of nucleic acids which consists of a sense primer that specifically hybridizes the partial DNA region including the base at position 1019 in the antisense strand of the connexin 37 gene whose base at position 1019 is T (thymine) and of an antisense primer that specifically hybridizes a partial region of the sense strand. The length of the partial DNA region to be amplified here is set accordingly in a range which is appropriate for its detection, and is for example, 50 bp to 200 bp, and preferably 80 bp to 150 bp. More concrete example of the set of nucleic acids for analyzing the connexin 37 (1019C→T) polymorphism for example may include a set containing the following sequences. Note here that an underlined part in the following sequences means a part corresponding to the polymorphism. Furthermore, in the sequence, N denotes any of A, T, C and G.

Sense primer

CTCAGAATGGCCAAAANCC : SEQ ID NO:15, or

CCTCAGAATGGCCAAAANTC : SEQ ID NO: 16

Antisense primer

GCAGAGCTGCTGGGACGA : SEQ ID NO: 17

Similarly, an example of a nucleic acid primer for analyzing the TNFα (-863C→A) polymorphism may include a set of nucleic acids including the following sequences.

Antisense primer

GGCCCTGTCTTCGTTAANGG: SEQ ID NO: 18, or

ATGGCCCTGTCTTCGTTAANTG: SEQ ID NO: 19

Sense primer

CCAGGGCTATGGAAGTCGAGTATC: SEQ ID NO: 20

Similarly, an example of a nucleic acid primer for analyzing the NADH/NADPH oxidase p22 phox (242C→T) polymorphism may include a set of nucleic acids including the following sequences.

Antisense primer

ACCACGGCGGTCATGNGC: SEQ ID NO: 21, or

ACCACGGCGGTCATGNAC: SEQ ID NO: 22

Sense primer

GCAGCAAAGGAGTCCCGAGT: SEQ ID NO: 23

Similarly, an example of a nucleic acid primer for analyzing the angiotensinogen (-6G→A) polymorphism may include a set of nucleic acids including the following sequences.

Antisense primer

CGGCAGCTTCTTCCCNCG: SEQ ID NO: 24. or

CGGCAGCTTCTTCCCNTG: SEQ ID NO: 25

Sense primer

CCACCCCTCAGCTATAAATAGG: SEQ ID NO: 26

Similarly, an example of a nucleic acid primer for analyzing the Apo E (-219G→T) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

GAATGGAGGAGGGTGTCTNGA: SEQ ID NO: 27, or

AGAATGGAGGAGGGTGTCTNTA: SEQ ID NO: 28

Antisense primer

CCAGGAAGGGAGGACACCTC: SEQ ID NO: 29

Similarly, an example of a nucleic acid primer for analyzing the PAF acetylhydrolase (994G→T) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

TTCTTTTGGTGGAGCAACNGT: SEQ ID NO: 30, or

ATTCTTTTGGTGGAGCAACNTT: SEQ ID NO: 31

Antisense primer

TCTTACCTGAATCTCTGATCTTCA: SEQ ID NO: 32

Similarly, an example of a nucleic acid primer for analyzing the Apo C-III (-482C→T) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

CGGAGCCACTGATGCNCG: SEQ ID NO: 33, or

CGGAGCCACTGATGCNTG: SEQ ID NO: 34

Antisense primer

TGTTTGGAGTAAAGGCACAGAA: SEQ ID NO: 35

Similarly, an example of a nucleic acid primer for analyzing the TSP4 (1186G→C) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

CGAGTTGGGAACGCACNCT: SEQ ID NO: 36, or

CGAGTTGGGAACGCACNGT: SEQ ID NO: 37

Antisense primer

GGTCTGCACTGACATTGATGAG: SEQ ID NO: 38

Similarly, an example of a nucleic acid primer for analyzing the IL-10 (-819T→C) polymorphism may include a set of nucleic acids

including the following sequences.

Sense primer

TACCCTTGTACAGGTGATGTANTA: SEQ ID NO: 39, or

TACCCTTGTACAGGTGATGTANCA: SEQ ID NO: 40

Antisense primer

ATAGTGAGCAAACTGAGGCACA: SEQ ID NO: 41

Similarly, an example of a nucleic acid primer for analyzing the IL-10 (-592A→C) polymorphism may include a set including the following sequences.

Antisense primer

CAGAGACTGGCTTCCTACANGA: SEQ ID NO: 42, or

CCAGAGACTGGCTTCCTACANTA: SEQ ID NO: 43

Sense primer

GCCTGGAACACATCCTGTGA: SEQ ID NO: 44

Similarly, an example of a nucleic acid primer for analyzing the stromelysin 1 (-1171/5A→6A) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

TTTGATGGGGGGAAAANAC: SEQ ID NO: 45, or

TTGATGGGGGGAAAANCC: SEQ ID NO: 46

Antisense primer

CCTCATATCAATGTGGCCAA: SEQ ID NO: 47

Similarly, an example of a nucleic acid primer for analyzing the PAI1 (-668/4G→5G) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

GGCACAGAGAGAGTCTGGACACG: SEQ ID NO: 48

Antisense primer

GGCCGCCTCCGATGATACA: SEQ ID NO: 49

Similarly, an example of a nucleic acid primer for analyzing the glycoprotein Ibα (1018C→T) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

CCCAGGGCTCCTGNCG: SEQ ID NO: 50, or

CCCCAGGGCTCCTGNTG: SEQ ID NO: 51

Antisense primer

TGAGCTTCTCCAGCTTGGGTG: SEQ ID NO: 52

Similarly, an example of a nucleic acid primer for analyzing the paraoxonase (584G→A) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

ACCCAAATACATCTCCCAGGANCG: SEQ ID NO: 53, or

AACCCAAATACATCTCCCAGGNCT: SEQ ID NO: 54

Antisense primer

GAATGATATTGTTGCTGTGGGAC: SEQ ID NO: 55

Similarly, an example of a nucleic acid primer for analyzing the Apo E (4070C→T) polymorphism may include a set of nucleic acids including the following sequences.

Sense primer

CCGATGACCTGCAGAANCG: SEQ ID NO: 56, or

GCCGATGACCTGCAGAANTG: SEQ ID NO: 57

Antisense primer

CGGCCTGGTACACTGCCAG: SEQ ID NO: 58

On the other hand, a concrete example of the probe can include:

as a probe for analyzing Apo C-III (-482C→T) polymorphism,

AGCCACTGATGCNCGGTCT: SEQ ID NO: 59, or

AGCCACTGATGCNTGGTCT: SEQ ID NO: 60,

as a probe for analyzing IL-10 (-819T→C) polymorphism,

GTACAGGTGATGTANTATCTCTGTG: SEQ ID NO: 61 or,

GTACAGGTGATGTANCATCTCTGTG: SEQ ID NO: 62, and

as a probe for analyzing PAI1 (-668/4G→5G) polymorphism,

TGGACACGTGGGGGAGTCAG: SEQ ID NO: 63, or

TGGACACGTGGGGAGTCAGC: SEQ ID NO: 64.

The above nucleic acid primers and nucleic acid probes are mere examples. Nucleic acid primers may contain a partially modified base sequence as long as they can carry out the aimed amplification reaction without inconvenience, while nucleic acid probes may contain a partially modified base sequence as long as they can carry out the aimed hybridization reaction without inconvenience. "Partially modified" herein means that part of bases is deleted, replaced, inserted, and/or added. The numbers of modified bases are for example one to seven, preferably one to five, and more preferably one to three. Note here that such a modification is made in the portions other than bases which correspond to the site of polymorphism, in principle. However, in the case where the polymorphism that is a subject of analysis is stromelysin 1 (-1171/5A→6A) polymorphism or PAI1 (-668/4G→5G) polymorphism, primers or probes obtained by modifying a part of base corresponding to a polymorphism site may be used.

As nucleic acids for polymorphism analysis (probes or primers), DNA fragments or RNA fragments are used accordingly in response to the analysis method employed. The base length of nucleic acids for polymorphism analysis may be sufficient if it exerts respective functions of each nucleic acid. Base lengths in the case of use as primers are for example, 10 to 50 bp, preferably 15 to 40 bp, and more preferably 15 to 30 bp.

Note here that in the case of use as primers, some mismatches to the sequence which constitutes the template may be admitted as long as the primer can specifically hybridize the subject for amplification and amplify the target DNA fragment. In the case of probes, some mismatches to the sequence which is subject to detection may be similarly admitted as long as the probe can specifically hybridize the sequence which is subject to detection. The numbers of mismatches are one to several, preferably one to five, and more preferably one to three.

Nucleic acids for polymorphism analysis (primers and probes) can be synthesized in accordance with known methods, e.g., phosphodiester method. Note here that textbooks (e.g., Molecular Cloning, Third Edition, Cold Spring Harbor Laboratory Press, New York) can be referred with respect to the design, synthesis, and others of nucleic acids for polymorphism analysis.

Nucleic acids for polymorphism analysis in the present invention can be labeled with labeling substances in advance. The use of such labeled nucleic acids allows, for example, the analysis of polymorphism by using the labeling amount in the product of amplification as a marker. Furthermore, by labeling two kinds of primers which were designed specifically amplify the partial DNA region in the gene of each genotype that constitute polymorphism

with labeling substances that are different from each other, the genotype of a nucleic acid sample can be discriminated according to the labeling substance and labeling amount to be detected based on the product of amplification. Concrete examples of detection methods using these labeled primers may include: a method for detecting polymorphism, comprising labeling, with fluorescein isocyanate and Texas red, two kinds of nucleic acid primers (allele-specific sense primers) that respectively and specifically hybridize the sense strand of each genotype constituting polymorphism; amplifying the partial DNA region including the site of polymorphism by using these labeled primers and the antisense primers that specifically hybridize the antisense strand; and measuring the labeling amount of each fluorescent substance in the product of amplification obtained. Note here that labeling of the antisense primer herein with for example, biotin allows the separation of the product of amplification by utilizing the specific binding between biotin and avidin.

Radioactive isotopes, for example, ^{32}P, and fluorescent substance, for example, fluorescein isothiocyanate, tetramethylrhodamine isothiocyanate, and Texas red, etc. can be exemplified as labeling substances to be used in labeling nucleic acids for polymorphism analysis. The 5' terminal labeling method using alkaline phosphatase and T4 polynucleotide kinase, the 3' terminal labeling method using T4 DNA polymerase and Klenow fragment, nicktranslation method, random primer method (Molecular Cloning, Third Edition, Chapter 9, Cold Spring Harbor Laboratory Press, New York), and the like can be exemplified as labeling methods.

The above-mentioned nucleic acids for polymorphism analysis

can be used also under a condition fixed to an insoluble support. Processing of an insoluble support to be used for the fixation to several forms such as chips and beads allows the more simplified analysis of polymorphism by using these fixed nucleic acids.

A nucleic acid sample can be prepared from blood, skin cells, mucous cells, hair, and others from the subject according to known extraction methods and purification methods. In the case of including the gene which is subject to the analysis of polymorphism, the genome DNA of arbitrary length can be used as a nucleic acid sample. Furthermore, it is not necessary to use a nucleic acid sample in which all genes subject to the analysis are present on one nucleic acid. That is to say, as a nucleic acid sample of the present invention, both material in which all genes subject to the analysis are present on one nucleic acid and material in which genes subject to the analysis are present separately on two or more nucleic acids can be used. Note here that material in a fragmented or partial condition may be accepted as long as the site of polymorphism to be analyzed is at least present, although genes subject to the analysis in a nucleic acid sample are not in a complete condition (i.e., a condition in which the full length of the gene is present).

Analysis of each gene polymorphism is carried out each by each of the gene polymorphism or a plurality or entire gene polymorphisms are carried out simultaneously. In the former case, for example, nucleic acid sample collected from the subjects is divided in accordance with the number of polymorphisms to be analyzed, and analysis of polymorphism is carried out individually. In the latter case, for example, analysis of polymorphism can be

carried out by DNA chip or micro-array. Note here that "simultaneousness" herein not only imply that all operations of the analysis process are conducted simultaneously but also include the case in which part of operations (e.g., operation to amplify nucleic acid, hybridization or detection of the probe) is conducted simultaneously.

Polymorphism of each gene can be analyzed by using mRNA which is a product of transcription of the gene which is subject to the analysis. After extracting and purifying mRNA of the gene which is subject to the analysis from blood, urine, and others of the subject, for example, polymorphism can be analyzed with mRNA as a starting material by conducting methods, e.g., Northern blotting method (Molecular Cloning, Third Edition, 7.42, Cold Spring Harbor Laboratory Press, New York), dot blotting method (Molecular Cloning, Third Edition, 7.46, Cold Spring Harbor Laboratory Press, New York), RT-PCR method (Molecular Cloning, Third Edition, 8.46, Cold Spring Harbor Laboratory Press, New York), and methods using the DNA chip (DNA array), and the like.

In addition, in the above-mentioned polymorphism, polymorphism involved with changes in amino acids can analyzed by using the expression product of gene that is a subject to analysis. In this case, material, even being partial protein or partial peptide, can be used as a sample for analysis as long as it contains amino acids which correspond to the site of polymorphism.

Analysis methods using these expression products of gene may include: a method for directly analyzing amino acids at the site of polymorphism, a method for immunologically analyzing

utilizing changes of three-dimensional structure, or the like. As the former, a well-known amino acid sequence analysis method (a method using Edman method) can be used. As the latter, ELISA (enzyme-linked immunosorbent assay) using the monoclonal antibody or polyclonal antibody which has binding activity specific to the expression product of gene which has any of genotypes that constitute polymorphism; radioimmunoassay, immunoprecipitation method, immunodiffusion method, and the like can be used.

Information about polymorphism to be obtained by conducting the detection methods of the present invention described above can be used to diagnose a genetic risk of myocardial infarction. That is to say, the present invention also provides a method for diagnosing a genetic risk of myocardial infarction, which comprises a step for determining the genotype in a nucleic acid sample based on information about polymorphism that was obtained by the above-detection methods, and a step for assessing a genetic risk of myocardial infarction based on the determined genotype of the nucleic acid sample. Herein, the determination of the genotype is typically to determine which genotype both alleles of nucleic acid samples have with respect to the polymorphism to be detected. In the case where the subject to be detected is connexin 37 (1019C→T) polymorphism, for example, typically, investigation on what type the connexin 37 gene in a nucleic acid sample is TT (the base at position 1019 is a homozygote of allele T), CT (the base at position 1019 is a heterozygote of allele C and allele T) and CC (the base at position 1019 is a homozygote of allele C) in a nucleic acid sample the connexin 37 gene is.

By considering the results obtained in Example mentioned

below, in order to enable a diagnosis of genetic risk of myocardial infarction with high accuracy and high predictability, for example, in the case of the connexin 37 (1019C→T) polymorphism, it is determined whether the genotype in a nucleic acid sample is TT or CT, or CC. Similarly, in the case of the TNFα (-863C→A) polymorphism, it is determined whether the genotype is AA or CA, or CC; in the case of NADH/NADPH oxidase p22 phox (242C→T) polymorphism, it is determined whether the genotype is TT or CT, or CC; in the case of angiotensinogen (-6G→A) polymorphism, it is determined whether the genotype is AA, or GA or GG; in the case of Apo E-219 (-219G→T) polymorphism, it is determined whether the genotype is TT, or GT or GG; in the case of PAF acetylhydrolase (994G→T) polymorphism, it is determined whether the genotype is TT or GT, or GG; in the case of Apo C-III (-482C→T) polymorphism, it is determined whether the genotype is TT, or CT or CC; in the case of TSP4 (1186G→C) polymorphism, it is determined whether the genotype is CC or GC, or GG; in the case of IL-10 (-819T→C) polymorphism, it is determined whether the genotype is CC, or CT or TT; in the case of IL-10 (-592A→C) polymorphism, it is determined whether the genotype is CC, or CA or AA; in the case of stromelysin 1 (-1171/5A→6A) polymorphism, it is determined whether the genotype is 6A/6A or 5A/6A, or 5A/5A; in the case of PAI1 (-668/4G→5G) polymorphism, it is determined whether the genotype is 5G/5G or 4G/5G, or 4G/4G; in the case of glycoprotein Ibα (1018C→T) polymorphism, it is determined whether the genotype is TT, or CT or CC; in the case of paraoxonase (584G→A) polymorphism, it is determined whether the genotype is AA, or GA or GG; and in the case of Apo E (4070C→T) polymorphism, it is determined whether the genotype is TT, or CT or CC.

Diagnosis of a genetic risk of myocardial infarction enables prediction of potentiality in that myocardial infraction might be developed in the future (susceptibility to development), that is, risk of development (predisposition to development). Furthermore, based on the objective indicator that is the genotype, it is possible to recognize myocardial infarction and to evaluate the state of disease. In other words, according to the diagnosing method of the present invention, it is possible to asses the risk of development of myocardial infarction or to evaluate the state of disease. Above all, it is extremely significant from the clinical viewpoint to carry out the assessment of the risk of development. It is advantageous because awareness in advance of the risk of development contributes to primary prevention of myocardial infarction and makes it possible to take an appropriate measurement.

Information to be obtained by a diagnostic method of the present invention can be used for selecting an appropriate treatment, improvement of prognosis, improvement in QOL (quality of life of patients), or reduction in risk of development.

By carrying out the diagnostic method of the present invention regularly, it is possible to monitor, for example, the risk of development of myocardial infarction. As a result of such monitoring, if the correlation between some external factors (environmental factors, administration of drugs, etc.) and the increase in the risk of development is found, such external factors are recognized as risk factors and it is thought that the risk of development can be reduced based on this information.

By utilizing the genetic information associated with the

development of myocardial infarction obtained by the present invention, it is possible to carry out a treatment (including a preventive treatment) for myocardial infarction. For example, as a result of carrying out the diagnostic method of the present invention, in the case where the polymorphism to be analyzed is a genotype to increase the risk of development of myocardial infarction, by introducing and expressing a gene having a genotype with low risk of development is introduced into a living body, the reduction of disease, suppression of development, and reduction of risk of development can be expected due to the expression of genes. The same treatment effect can be expected by a method including: introducing antisense strand with respect to mRNA of gene having a genotype with high risk of development and suppressing the expression of the mRNA.

The introduction of gene or antisense strand can be carried out by a method, for example, a method using a plasmid for gene introduction or a virus vector, electroporation (Potter,H. et al., Proc. Natl. Acad. Sci. U.S.A. 81, 7161-7165(1984), an ultrasonic microbubble (Lawrie, A., et al. Gene Therapy 7, 2023-2027 (2000)), lipofection (Felgner, P.L. et al., Proc. Natl. Acad. Sci. U.S.A. 84, 7413-7417 (1984)), microinjection (Graessmann, M. & Graessmann, A., Proc. Natl. Acad. Sci. U.S.A. 73,366-370(1976)), and the like. By utilizing these methods, desired genes, etc. can be directly introduced (in vivo method) or indirectly introduced (ex vivo method).

The second aspect of the present invention provides kits to be used in the above-mentioned detecting method or diagnostic method in the present invention (kits for detecting the genotype

or kits for diagnosing myocardial infarction). Such kits contain nucleic acids (nucleic acid for polymorphism analysis) for analyzing two or more polymorphisms selected from the group consisting of polymorphisms described in (1) to (10) above; or such kits contain nucleic acids (nucleic acid for polymorphism analysis) for analyzing two or more polymorphisms selected from the group consisting of polymorphisms described in (11) to (15) above. As further embodiment, kits are constructed, which contains nucleic acid for polymorphism analysis described in (15) above.

In the analysis methods by which it is applied (a method which utilizes PCR using the above-mentioned allele-specific nucleic acids and the like, PCR-RFLP method, PCR-SSCP method, TaqMan-PCR method, Invader method, etc.), nucleic acids for polymorphism analysis are designed as materials which can specifically amplifies (primer) or specifically detect (probe) the DNA region containing the polymorphism portion to be analyzed or mRNA which corresponds to the region. Concrete examples of kits to be provided according to the present invention are described below.

A kit for detecting the genotype, comprising two or more nucleic acids selected from the group consisting of the below-mentioned (1) to (10):

(1) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 1019 of the connexin 37 gene whose base at position 1019 is C, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 1019 of the connexin 37 gene whose base at position 1019 is T:

(2) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -863 of the tumor necrosis factor α gene whose base at position -863 is C, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -863 of the tumor necrosis factor α gene whose base at position -863 is A:

(3) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 242 of the NADH/NADPH oxidase p22 phox gene whose base at position 242 is C, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 242 of the NADH/NADPH oxidase p22 phox gene whose base at position 242 is T:

(4) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -6 of the angiotensinogen gene whose base at position -6 is G, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -6 of the angiotensinogen gene whose base at position -6 is A:

(5) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -219 of the apolipoprotein E gene whose base at position -219 is G, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -219 of the apolipoprotein E gene whose base at position -219 is T:

(6) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 994 of the platelet-activating factor acetylhydrolase gene whose base at position 994 is G, or a nucleic acid having a sequence which is

complementary to the partial DNA region containing the base at position 994 of the platelet-activating factor acetylhydrolase gene whose base at position 994 is T:

(7) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -482 of the apolipoprotein C-III gene whose base at position -482 is C, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -482 of the apolipoprotein C-III gene whose base at position -482 is T:

(8) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 1186 of the thrombospondin 4 gene whose base at position 1186 is G, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 1186 of the thrombospondin 4 gene whose base at position 1186 is C:

(9) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -819 of the interleukin-10 gene whose base at position -819 is T, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -819 of the interleukin-10 gene whose base at position -819 is C: and

(10) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -592 of the interleukin-10 gene whose base at position -592 is A, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position -592 of the interleukin-10 gene whose base at position -592 is C.

In the above mention, kits are constructed by selecting two or more nucleic acids from the group consisting of (1) to (10). However, kits may be constructed by making a group consisting of

two or more nucleic acids arbitrarily selected from (1) to (10) and selecting two or more nucleic acids from such a group. For example, kits are constructed by selecting two or more nucleic acids from the group consisting of (1), (5), (6), (8), (9) and (10) (nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits are constructed by selecting two or more nucleic acids from the group consisting of (1), (5), (6), (8) and (9) (nucleic acids for polymorphism analysis with five highest odds ratios in Example mentioned below).

A kit for detecting the genotype, comprising two or more nucleic acids selected from the group consisting of the following (11) to (15):

(11) a nucleic acid having a sequence which is complementary to the partial DNA region containing the part of sequence of the stromelysin 1 gene in which five A successively exist in the 3' direction from the position -1171, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the part of sequence of the stromelysin 1 gene in which six A successively exist in the 3' direction from the position -1171;

(12) a nucleic acid having a sequence which is complementary to the partial DNA region containing the part of sequence of the plasminogen activator inhibitor 1 gene in which four G successively exist in the 3' direction from the position -668, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the part of sequence of the plasminogen activator inhibitor 1 gene in which five G successively exist in the 3' direction from the position -668 in the 3' direction;

(13) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 1018

of the glycoprotein Ibα gene whose base at position 1018 is C, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 1018 of the glycoprotein Ibα gene whose base at position 1018 is T;

(14) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 584 of the paraoxonase gene whose base at position 584 is G, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 584 of the paraoxonase gene whose base at position 584 is A; and

(15) a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 4070 of the apolipoprotein E gene whose base at position 4070 is C, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 4070 of the apolipoprotein E gene whose base at position 4070 is T.

In the above mention, kits are constructed by selecting two or more nucleic acids from the group consisting of (11) to (15). However, kits may be constructed by making a group consisting of two or more nucleic acids arbitrarily selected from (11) to (15) and selecting two or more nucleic acids from such a group. For example, kits are constructed by selecting two or more nucleic acids from the group consisting of (11), (12), (14) and (15) (nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits are constructed by selecting two or more nucleic acids from the group consisting of (11), (12) and (15) (nucleic acids for polymorphism analysis with three highest odds ratios in Example mentioned below).

A kit for detecting the genotype comprising the following

nucleic acid:

a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 4070 of the apolipoprotein E gene whose base at position 4070 is C, or a nucleic acid having a sequence which is complementary to the partial DNA region containing the base at position 4070 of the apolipoprotein E gene whose base at position 4070 is T.

A kit for detecting the genotype, comprising two or more sets of nucleic acids selected from the group consisting of the following (1) to (10):

(1) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1019 of the connexin 37 gene only in the case where the base at position 1019 of the connexin 37 gene in a nucleic acid sample is C, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1019 of the connexin 37 gene only in the case where the base at position 1019 of the connexin 37 gene in a nucleic acid sample is T;

(2) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -863 of the tumor necrosis factor α gene only in the case where the base at position -863 of the tumor necrosis factor α gene in a nucleic acid sample is C, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -863 of the tumor necrosis factor α gene only in the case where the base at position -863 of the tumor necrosis factor α gene in a nucleic acid sample is A;

(3) a set of nucleic acids which is designed to specifically

amplify the partial DNA region containing the base at position 242 of the NADH/NADPH oxidase p22 phox gene only in the case where the base at position 242 of the NADH/NADPH oxidase p22 phox gene in a nucleic acid sample is C, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 242 of the NADH/NADPH oxidase p22 phox gene only in the case where the base at position 242 of the NADH/NADPH oxidase p22 phox gene in a nucleic acid sample is T;

(4) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -6 of the angiotensinogen gene only in the case where the base at position -6 of the angiotensinogen gene in a nucleic acid sample is G, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -6 of the angiotensinogen gene only in the case where the base at position -6 of the angiotensinogen gene in a nucleic acid sample is A;

(5) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -219 of the apolipoprotein E gene only in the case where the base at position -219 of the apolipoprotein E gene in a nucleic acid sample is G, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -219 of the apolipoprotein E gene only in the case where the base at position -219 of the apolipoprotein E gene in a nucleic acid sample is T;

(6) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 994 of the platelet-activating factor acetylhydrolase gene only in the case where the base at position 994 of the platelet-activating

factor acetylhydrolase gene in a nucleic acid sample is G, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 994 of the platelet-activating factor acetylhydrolase gene only in the case where the base at position 994 of the platelet-activating factor acetylhydrolase gene in a nucleic acid sample is T;

(7) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -482 of the apolipoprotein C-III gene only in the case where the base at position -482 of the apolipoprotein C-III gene in a nucleic acid sample is C, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -482 of the apolipoprotein C-III gene only in the case where the base at position -482 of the apolipoprotein C-III gene in a nucleic acid sample is T;

(8) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1186 of the thrombospondin 4 gene only in the case where the base at position 1186 of the thrombospondin 4 gene in a nucleic acid sample is G, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1186 of the thrombospondin 4 gene only in the case where the base at position 1186 of the thrombospondin 4 gene in a nucleic acid sample is C;

(9) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -819 of the interleukin-10 gene only in the case where the base at position -819 of the interleukin-10 gene in a nucleic acid sample is T, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position

-819 of the interleukin-10 gene only in the case where the base at position -819 of the interleukin-10 gene in a nucleic acid sample is C; and

(10) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -592 of the interleukin-10 gene only in the case where the base at position -592 of the interleukin-10 gene in a nucleic acid sample is A, or a set of nucleic acids which, is designed to specifically amplify the partial DNA region containing the base at position -592 of the interleukin-10 gene only in the case where the base at position -592 of the interleukin-10 gene in a nucleic acid sample is C;

In the above mention, kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (1) to (10). However, kits may be constructed by making a group consisting of two or more sets of nucleic acids arbitrarily selected from (1) to (10) and selecting two or more sets of nucleic acids from such a group. For example, kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (1), (5), (6), (8), (9) and (10) (nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (1), (5), (6), (8) and (9) (nucleic acids for polymorphism analysis with five highest odds ratios in Example mentioned below).

A kit for detecting the genotype, comprising two or more sets of nucleic acids selected from the group consisting of the following (11) to (15):

(11) a set of nucleic acids which is designed to specifically

amplify the partial DNA region containing the part of sequence of the stromelysin 1 gene only in the case where five A exist successively in the 3' direction from the position -1171 in the stromelysin 1 gene in a nucleic acid sample, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the part of sequence of the stromelysin 1 gene only in the case where six A exist successively in the 3' direction from the position -1171 in the stromelysin 1 gene in a nucleic acid sample;

(12) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the part of sequence of the plasminogen activator inhibitor 1 gene only in the case where four G exist successively in the 3' direction from the position -668 in the plasminogen activator inhibitor 1 gene in a nucleic acid sample, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the part of sequence of the plasminogen activator inhibitor 1 gene only in the case where five G exist successively in the 3' direction from the position -668 in the plasminogen activator inhibitor 1 gene in a nucleic acid sample;

(13) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1018 of the glycoprotein Ibα gene only in the case where the base at position 1018 of the glycoprotein Ibα gene in a nucleic acid sample is C, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1018 of glycoprotein Ibα gene only in the case where the base at position 1018 of the glycoprotein Ibα gene in a nucleic acid sample is T;

(14) a set of nucleic acids which is designed to specifically

amplify the partial DNA region containing the base at position 584 of the paraoxonase gene only in the case where the base at position 584 of the paraoxonase gene in a nucleic acid sample is G, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 584 of the paraoxonase gene only in the case where the base at position 584 of paraoxonase gene in a nucleic acid sample is A; and

(15) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene only in the case where the base at position 4070 of the apolipoprotein E gene in a nucleic acid sample is C, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene only in the case where the base at position 4070 of the apolipoprotein E gene in a nucleic acid sample is T.

In the above mention, kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (11) to (15). However, kits may be constructed by making a group consisting of two or more sets of nucleic acids arbitrarily selected from (11) to (15) and selecting two or more sets of nucleic acids from such a group. For example, kits may be constructed by selecting two or more sets of nucleic acids from the group consisting of (11), (12), (14) and (15) (sets of nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits may be constructed by selecting two or more sets of nucleic acids from the group consisting of (11), (12) and (15) (sets of nucleic acid for polymorphism analysis with three highest odds ratios in Example mentioned below).

A kit for detecting the genotype, comprising the following set of nucleic acids:

a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene only in the case where the base at position 4070 of the apolipoprotein E gene in a nucleic acid sample is C, or a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene only in the case where the base at position 4070 of the apolipoprotein E gene in a nucleic acid sample is T.

A kit for detecting the genotype, comprising two or more sets of nucleic acids selected from the group consisting of the following (1) to (10):

(1) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1019 of the connexin 37 gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position 1019 of the connexin 37 gene whose base at position 1019 is C and/or a sense primer that specifically hybridizes the partial DNA region containing the base at position 1019 in the connexin 37 gene whose gene at position 1019 is T and of an antisense primer that specifically hybridizes a partial portion of the connexin 37 gene;

(2) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -863 of the tumor necrosis factor α gene and which consists of an antisense primer that specifically hybridizes the partial DNA

region containing the base at position -863 of the tumor necrosis factor α gene whose base at position -863 is C and/or an antisense primer that specifically hybridizes the partial DNA region containing the base at position -863 in the tumor necrosis factor α gene whose gene at position -863 is A and of a sense primer that specifically hybridizes a partial portion of the tumor necrosis factor α gene;

(3) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 242 of the NADH/NADPH oxidase p22 phox gene and which consists of an antisense primer that specifically hybridizes the partial DNA region containing the base at position -863 of the NADH/NADPH oxidase p22 phox gene whose base at position 242 is C and/or an antisense primer that specifically hybridizes the partial DNA region containing the base at position 242 in the NADH/NADPH oxidase p22 phox gene whose gene at position 242 is T and of a sense primer that specifically hybridizes a partial portion of the NADH/NADPH oxidase p22 phox gene;

(4) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -6 of the angiotensinogen gene and which consists of an antisense primer that specifically hybridizes the partial DNA region containing the base at position -6 of the angiotensinogen gene whose base at position -6 is G and/or an antisense primer that specifically hybridizes the partial DNA region containing the base at position -6 in the angiotensinogen gene whose gene at position -6 is A and of a sense primer that specifically hybridizes a partial portion of the angiotensinogen gene;

(5) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position

-219 of the apolipoprotein E gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position -219 of the apolipoprotein E gene whose base at position -219 is G and/or a sense primer that specifically hybridizes the partial DNA region containing the base at position -219 in the apolipoprotein E gene whose gene at position -219 is T and of an antisense primer that specifically hybridizes a partial portion of the apolipoprotein E gene;

(6) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 994 of the platelet-activating factor acetylhydrolase gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position 994 of the platelet-activating factor acetylhydrolase gene whose base at position 994 is G and/or a sense primer that specifically hybridizes the partial DNA region containing the base at position 994 in the platelet-activating factor acetylhydrolase gene whose gene at position 994 is T and of an antisense primer that specifically hybridizes a partial portion of the platelet-activating factor acetylhydrolase gene;

(7) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -482 of the apolipoprotein C-III gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position -482 of the apolipoprotein C-III gene whose base at position -482 is C and/or a sense primer that specifically hybridizes the partial DNA region containing the base at position -482 in the apolipoprotein C-III gene whose gene at position -482 is T and of an antisense primer that specifically hybridizes a partial portion of the apolipoprotein C-III gene;

(8) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1186 of the thrombospondin 4 gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position 1186 of the thrombospondin 4 whose base at position 1186 is G and/or a sense primer that specifically hybridizes the partial DNA region containing the base at position 1186 in the thrombospondin 4 gene whose gene at position 1186 is C and of an antisense primer that specifically hybridizes a partial portion of the thrombospondin 4 gene;

(9) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -819 of the interleukin-10 gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position -819 of the interleukin-10 whose base at position -819 is T and/or a sense primer that specifically hybridizes the partial DNA region containing the base at position -819 in the interleukin-10 gene whose gene at position -1186 is C and of an antisense primer that specifically hybridizes a partial portion of the interleukin-10 gene; and

(10) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position -592 of the interleukin-10 gene and which consists of an antisense primer that specifically hybridizes the partial DNA region containing the base at position -592 of the interleukin-10 whose base at position -592 is A and/or an antisense primer that specifically hybridizes the partial DNA region containing the base at position -592 in the interleukin-10 gene whose gene at position -592 is C and of a sense primer that specifically hybridizes a partial portion of the interleukin-10 gene.

In the above mention, kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (1) to (10). However, kits may be constructed by making a group consisting of two or more sets of nucleic acids arbitrarily selected from (1) to (10) and selecting two or more sets of nucleic acids from such a group. For example, kits are constructed by selecting two or more nucleic acids from the group consisting of (1), (5), (6), (8), (9) and (10) (sets of nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (1), (5), (6), (8) and (9) (sets of nucleic acids for polymorphism analysis with five highest odds ratios in Example mentioned below).

A kit for detecting the genotype, comprising two or more sets of nucleic acids selected from the group consisting of the following (11) to (15):

(11) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing a part of polymorphism at position -1171 of the stromelysin 1 gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the corresponding sequence of the stromelysin 1 gene in which five A successively exist in the 3' direction from the position -1171, and/or a sense primer that specifically hybridizes the partial DNA region containing the corresponding sequence of the streomelysin 1 in which six A successively exist in the 3' direction from the position -1171, and an antisense primer that specifically hybridizes a part of region of the stromelysin 1 gene;

(12) a set of nucleic acids consisting of a pair of primers which

are designed to specifically amplify the partial DNA region containing a part of polymorphism at position -668 of the plasminogen activator inhibitor 1 gene, as well as a probe that specifically hybridizes the partial DNA region containing the corresponding sequence in the plasminogen activator inhibitor 1 gene in which four G successively exist in the 3' direction from the position -668, and/or a probe that specifically hybridizes the partial DNA region containing the corresponding sequence in the plasminogen activator inhibitor 1 gene in which five G successively exist in the 3' direction from the position -668;

(13) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 1018 of the glycoprotein Ibα gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position 1018 of the glycoprotein Ibα gene in which the base at position 1018 is C, and/or a sense primer that specifically hybridizes the partial DNA region of the glycoprotein Ibα gene in which the base at position 1018 is T, and an antisense primer that specifically hybridizes a part of region of the glycoprotein Ibα gene;

(14) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 584 of the paraoxonase gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position 584 of the paraoxonase gene in which the base at position 584 is G, and/or a sense primer that specifically hybridizes the partial DNA region of the paraoxonase gene in which the base at position 584 is A, and an antisense primer that specifically hybridizes a part of region of the paraoxonase gene; and

(15) a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene and which consists of a sense primer that specifically hybridizes the partial DNA region containing the base at position 4070 of the apolipoprotein E gene in which the base at position 4070 is C, and/or a sense primer that specifically hybridizes the partial DNA region of the apolipoprotein E gene in which the base at position 4070 is T, and an antisense primer that specifically hybridizes a part of region of the apolipoprotein E gene;

In the above mention, kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (11) to (15). However, kits may be constructed by making a group consisting of two or more sets of nucleic acids arbitrarily selected from (11) to (15) and selecting two or more sets of nucleic acids from such a group. For example, kits are constructed by selecting two or more nucleic acids from the group consisting of (11), (12), (14) and (15) (sets of nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (11), (12) and (15) (sets of nucleic acids for polymorphism analysis with three highest odds ratios in Example mentioned below).

A kit for detecting the genotype, comprising the following a set of nucleic acids,

a set of nucleic acids which is designed to specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene and which consists of a sense primer that specifically hybridizes the partial DNA region

containing the base at position 4070 of the apolipoprotein E gene in which the base at position 4070 is C, and/or a sense primer that specifically hybridizes the partial DNA region of the apolipoprotein E gene in which the base at position 4070 is T, and an antisense primer that specifically hybridizes a part of region of the apolipoprotein E gene.

A kit for detecting the genotype comprising two or more sets of nucleic acids selected from the group consisting of the following (1) to (10);

(1) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position 1019 in the antisense strand of the connexin 37 gene whose base at position 1019 is C and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position 1019 in the antisense strand of the connexin 37 gene whose base at position 1019 is T and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the connexin 37 gene and that can specifically amplify the partial DNA region containing the base at position 1019 of the connexin 37 in concurrent use with the above first or second nucleic acid;

(2) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position -863 in the sense strand of the tumor necrosis factor α gene whose base at position -863 is C and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position -863 in the sense strand of the tumor necrosis factor

α gene whose base at position -863 is A and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the antisense strand of the tumor necrosis factor α gene and that can specifically amplify the partial DNA region containing the base at position -863 of the tumor necrosis factor α in concurrent use with the above first or second nucleic acid;

(3) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position 242 in the sense strand of the NADH/NADPH oxidase p22 phox gene whose base at position 242 is C and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position 242 in the sense strand of the NADH/NADPH oxidase p22 phox gene whose base at position 242 is T and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the antisense strand of the NADH/NADPH oxidase p22 phox gene and that can specifically amplify the partial DNA region containing the base at position 242 of the NADH/NADPH oxidase p22 phox in concurrent use with the above first or second nucleic acid;

(4) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position -6 in the sense strand of the angiotensinogen gene whose base at position -6 is G and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position -6 in the sense strand of the angiotensinogen gene whose base at position -6 is A and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial

region of the antisense strand of the angiotensinogen gene and that can specifically amplify the partial DNA region containing the base at position -6 of the angiotensinogen in concurrent use with the above first or second nucleic acid;

(5) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position -219 in the antisense strand of the apolipoprotein E gene whose base at position -219 is G and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position -219 in the antisense strand of the apolipoprotein E gene whose base at position -219 is T and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the apolipoprotein E gene and that can specifically amplify the partial DNA region containing the base at position -219 of the apolipoprotein E in concurrent use with the above first or second nucleic acid;

(6) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position 994 in the antisense strand of the platelet-activating factor acetylhydrolase gene whose base at position 994 is G and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position 994 in the antisense strand of the platelet-activating factor acetylhydrolase gene whose base at position 994 is T and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the platelet-activating factor acetylhydrolase gene and that can specifically amplify the

partial DNA region containing the base at position 994 of the platelet-activating factor acetylhydrolase gene in concurrent use with the above first or second nucleic acid;

(7) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position -482 in the antisense strand of the apolipoprotein C-III gene whose base at position -482 is C, of a second nucleic acid that specifically hybridizes a partial region containing the base at position -482 in the antisense strand of the apolipoprotein C-III gene whose base at position -482 is T, of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the apolipoprotein C-III gene and that can specifically amplify the partial DNA region containing the base at position -482 of the apolipoprotein C-III gene in concurrent use with the above first or second nucleic acid, of the fourth nucleic acid that specifically hybridizes the nucleic acid amplified by the use of the first and third nucleic acids; and of the fifth nucleic acid that specifically hybridizes the nucleic acid amplified by the use of the second and third nucleic acids;

(8) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position 1186 in the antisense strand of the thrombospondin 4 gene whose base at position 1186 is G and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position 1186 in the antisense strand of the thrombospondin 4 gene whose base at position 1186 is C and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the thrombospondin 4 gene and that can specifically amplify the partial

DNA region containing the base at position 1186 of the thrombospondin 4 gene in concurrent use with the above first or second nucleic acid;

(9) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position -819 in the antisense strand of the interleukin-10 gene whose base at position -819 is T, of a second nucleic acid that specifically hybridizes a partial region containing the base at position -819 in the antisense strand of the interleukin-10 gene whose base at position -819 is C, of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the interleukin-10 gene and that can specifically amplify the partial DNA region containing the base at position -819 of the interleukin-10 gene in concurrent use with the above first or second nucleic acid, of the fourth nucleic acid that specifically hybridizes the nucleic acid amplified by the use of the first and third nucleic acids; and of the fifth nucleic acid that specifically hybridizes the nucleic acid amplified by the use of the second and third nucleic acids; and

(10) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing the base at position -592 in the sense strand of the interleukin-10 gene whose base at position -592 is A and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing the base at position -592 in the sense strand of the interleukin-10 gene whose base at position -592 is C and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the antisense strand of the interleukin-10 gene and that can specifically amplify the partial DNA region

containing the base at position -592 of the interleukin-10 gene in concurrent use with the above first or second nucleic acid.

In the above mention, kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (1) to (10). However, kits may be constructed by making a group consisting of two or more sets of nucleic acids arbitrarily selected from (1) to (10) and selecting two or more sets of nucleic acids from such a group. For example, kits may be constructed by selecting two or more sets of nucleic acids from the group consisting of (1), (5), (6), (8), (9) and (10) (sets of nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits may be constructed by selecting two or more sets of nucleic acids from the group consisting of (1), (5), (6), (8) and (9) (sets of nucleic acids for polymorphism analysis with five highest odds ratios in Example mentioned below).

A kit for detecting the genotype, comprising two or more sets of nucleic acids selected from the group consisting of the following (11) to (15):

(11) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing a sequence which corresponds to the part of sequence in the antisense strand of the stromelysin 1 gene in which five A successively exist in the 3′ direction from the position -1171 and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing a sequence which corresponds to the part of sequence in the antisense strand of the stromelysin 1 gene in which six A successively exist in the 3′ direction from the position -1171 and that is labeled with a second labeling substance, and of a third nucleic acid that

specifically hybridizes a partial region of the sense strand of the stromelysin 1 gene and that can specifically amplify the partial DNA region containing the base at position -1171 of the stromelysin 1 gene in concurrent use with the above first or second nucleic acid;

(12) a set of nucleic acids which consists of a pair of nucleic acids (a first nucleic acid and a second nucleic acid) that is designed to specifically amplify the partial DNA region containing a part of polymorphism at position -668 of the plasminogen activator inhibitor 1 gene, of a third nucleic acid that specifically hybridizes the nucleic acid which is obtained by amplification using plasminogen activator inhibitor 1 gene in which four G successively exist in the 3' direction from the position -668 as a template and the set of nucleic acids, and of a four nucleic acid that specifically hybridizes a nucleic acid which is obtained by amplification using plasminogen activator inhibitor 1 gene in which five G successively exist in the 3' direction from the position -668 as a template and the set of nucleic acids;

(13) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the base at position 1018 in the antisense strand of the glycoprotein Ibα gene whose base at position 1018 is C and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the base at position 1018 in the antisense strand of the glycoprotein Ibα gene whose base at position 1018 is T and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the glycoprotein Ibα gene and that can specifically amplify the partial DNA region containing

the base at position 1018 of the glycoprotein Ibα gene in concurrent use with the above first or second nucleic acid;

(14) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the base at position 584 in the antisense strand of the paraoxonase gene whose base at position 584 is G and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the base at position 584 in the antisense strand of the paraoxonase gene whose base at position 584 is A and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the paraoxonase gene and that can specifically amplify the partial DNA region containing the base at position 584 of the paraoxonase gene in concurrent use with the above first or second nucleic acid; and

(15) a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the part of sequence in the antisense strand of the apolipoprotein E gene whose base at position 4070 is C and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the part of sequence in the antisense strand of the apolipoprotein E gene whose base at position 4070 is T and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the glycoprotein Ibα gene and that can specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene in concurrent use with the above first or second nucleic acid.

In the above mention, kits are constructed by selecting two or more sets of nucleic acids from the group consisting of (11) to (15). However, kits may be constructed by making a group consisting of two or more sets of nucleic acids arbitrarily selected from (11) to (15) and selecting two or more sets of nucleic acids from such a group. For example, kits are constructed by selecting two or more nucleic acids from the group consisting of (11), (12), (14) and (15) (sets of nucleic acids for polymorphism analysis with odds ratio of one or more in Example mentioned below), or kits are constructed by selecting two or more nucleic acids from the group consisting of (11), (12) and (15) (sets of nucleic acids for polymorphism analysis with three highest odds ratios in Example mentioned below).

A kit for detecting the genotype, comprising the following sets of nucleic acids:

a set of nucleic acids which consists of a first nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the part of sequence in the antisense strand of the apolipoprotein E gene whose base at position 4070 is C and that is labeled with a first labeling substance, of a second nucleic acid that specifically hybridizes a partial region containing a base which corresponds to the part of sequence in the antisense strand of the apolipoprotein E gene whose base at position 4070 is T and that is labeled with a second labeling substance, and of a third nucleic acid that specifically hybridizes a partial region of the sense strand of the glycoprotein Ibα gene and that can specifically amplify the partial DNA region containing the base at position 4070 of the apolipoprotein E gene in concurrent use with the above first or second nucleic acid.

In the above-mentioned kits, one or two or more of reagents (buffer, reagent for reaction, and reagent for detection, etc.) may be combined in response to the usage of the kit.

The present invention is hereinafter explained in more detail by way of Examples.

[Example 1] Selection of gene polymorphism

By using several kinds of common databases including PubMed [National Center for Biological Information (NCBI)], Online Mendelian inheritance in Men (NCBI), Single Nucleotide Polymorphism (NCBI), etc., from a comprehensive viewpoint including vascular biology, platelet-leucocyte biology, congealing fibrinogenolysis system, a metabolic factor such as lipid, sugar, etc., 71 genes which were estimated to be associated with coronary arteriosclerosis, coronary artery spasm, hypertension, diabetes, hyperlipidemia, etc. were extracted from genes which had been previously reported. Furthermore, in the polymorphisms existing in these genes, 112 polymorphisms including polymorphisms which exist in promoter regions or exons, or polymorphisms which were located in splice donor sites or acceptor sites and which were expected to be associated with the functional changes of gene products were selected (Figs. 1 and 2).

[Example 2] Determination of gene polymorphism

Subjects were 5061 Japanese males and females (3309 males and 1752 females) who visited as outpatients or were hospitalized in 15 participating institutes between July 1994 and December 2001. 2819 subjects (2003 males and 816 females) had myocardial infarction. All subjects were subjected to coronary angiography and left

ventriculography. Diagnosis of myocardial infarction was carried out based on electrocardiographic change and increases in serum CK, GOT and LDH. Confirmed diagnosis of myocardial infarction was determined based on abnormality in wall motion in left ventriculography and stenosis of left main coronary artery or major coronary arteries corresponding thereto.

Controls were 2242 people (1306 males and 936 females) who visited the participating institutes and had at least one of the conventional risk factors of coronary artery diseases, i.e., smoking (10 cigarettes or more per day), obesity (body mass index $\geq 26\ kg/m^2$), hypertension (systolic blood pressure ≥ 140 mmHg or/and diastolic blood pressure ≥ 90 mmHg), diabetes (fasting blood sugar ≥ 126 mg/dL or/and hemoglobin A1c $\geq 6.5\%$), hyperlipidemia (total cholesterol in serum ≥ 220 mg/dL), hyperuricemia (male: uric acid ≥ 7.7 mg/dL, female: uric acid ≥ 5.5 mg/dL) but did not have coronary artery disease. In these controls, resting electrocardiogram showed normal, and also in exercise tolerance test, no change showing myocardial ischemia was observed.

From each of the subjects, 7 mL of venous blood was collected in a tube containing 50 mmol/L EDTA-2Na and genome DNA was extracted by using DNA extraction kit (Qiagen, Chatsworth, CA). 71 candidate genes 112 polymorphisms were determined by allele specific primer-probe measurement system (Toyobo Gene Analysis, Tsuruga, Japan) by fluorescence method and spectrometry (see Figs. 3 and 4). DNA fragment containing a polymorphism site was amplified by polymerase chain reaction (PCR) by using two kinds of allele specific sense primers (or antisense primers) whose 5' end were labeled with fluorescein isothiocyanate (FITC) or Texas red (TxR)

and an antisense primer (or a sense primer) whose 5' end was labeled with biotin. Alternatively, DNA fragment containing polymorphism site was amplified by PCR by using two kinds of allele specific sense primer and antisense primer whose 5' end was labeled with biotin or by using a sense primer and antisense primer whose 5' end was labeled with biotin. The reaction solution (25 μL) contained 20 ng of DNA, 5 pmol of each primer, 0.2 mmol/L of each deoxynucleoside triphosphate (dATP, dGTP, dCTP and dTTP), 1-4 mmol/L of $MgCl_2$, 1 U DNA polymerase (rTaq or KODplus; Toyobo Co., Ltd. Osaka, Japan), and each DNA polymerase buffer was used. Amplification protocol included: initial degeneration at 95° C for 5 minutes; 35-45 cycles of degeneration at 95° C for 30 minutes, annealing at 55-67.5° C for 30 seconds, and extension at 72° C for 30 seconds; and final extension at 72° C for 2 minutes.

In the determination of the genotype by fluorescent method, amplified DNA was incubated in a solution containing streptavidin binding magnetic beads in a 96-well plate at room temperature. This plate was disposed on a magnetic stand and supernatant was collected from each well and transferred into each well of the 96-well plate containing 0.01 M NaOH, followed by measuring fluorescence by microplate reader at excitation wavelength and emission wavelength of 485 nm and 538 nm for FITC and at excitation wavelength and emission wavelength of 584 nm and 612 nm for TxR. Furthermore, in the determination of the genotype by spectrometry, amplified DNA was denatured by 0.3 M NaOH and hybridized by using a hybridization buffer containing any of allele specific probe fixed to the bottom surface of each well of the 96-well plate and 35-40% formamide at 37° C for 30 minutes. The well was thoroughly washed and then alkaline phosphatase binding streptavidin was added

to each well and the plate was shaken at 37° for 15 minutes. The well was washed again and a solution containing 0.8 mM 2-(4-iodophenyl)-3-(4-nitrophenyl)-5-(2,4-disulfophenyl)-2H-tetrazolium (monosodium salt) and 0.4 mM 5-bromo-4-chloro-3-indolyl phosphate p-toluidine salt was added, followed by measuring the absorbance (450 nm).

In order to confirm the accuracy of the determination of the genotype, DNA samples of 50 people were selected at random, and the samples were subjected to PCR-restriction fragment length polymorphism (PCR-RFLP) method or direct sequence determination for nucleic acid of PCR product. In any samples, the genotype determined by the allele specific primer-probe measurement system were the same as those determined by PCR-polymerase chain reaction-restriction fragment length polymorphism method or direct determination method of DNA sequence.

Note here that statistical analysis in the following association study was carried out as follows. First of all, data were shown in average ± standard deviation. Comparison of clinical data was carried out between patients with myocardial infarction and controls by using an unpaired Student's *t* test or a Mann-Whitney *U* test. Data in three groups were compared by way of a one-way analysis of variance and a Scheffe's post-hoc test or a Kruskal-Wallis test. Qualitative data were tested by a chi-square test. The allele frequency was estimated by a gene counting method and its deviation from the Hardy-Weinberg equilibrium was tested by a chi-square test. Furthermore, a multivariate logistic regression analysis in which risk factors were corrected was carried out. Myocardial infarction was used as a dependent variable, and

age, body mass index (BMI), smoking condition (0 = no smoking, 1 = smoking), metabolic factor (0 = without histories of hypertension, diabetes, hypercholesteremia, hyperuricemia, 1 = with histories above) and genotype of respective polymorphisms were used as independent variables. The respective genotypes were analyzed for dominant, recessive, additive genetic models, and P value, odds ratio, 95% confidence interval (CI) were calculated. In the combination of analysis of the genotype, odds ratio of each the genotype was calculated by a stepwise forward selection method of logistic regression analysis.

[Example 3] Selection of polymorphism associated with myocardial infarction and development of method for diagnosing myocardial infarction

Firstly, screening related analyses regarding 71 genes 112 polymorphisms were carried out for 451 males (myocardial infarction: 219, control: 232) and 458 females (myocardial infarction: 226, control: 232). These cases were selected at random from entire 5061 cases.

Background data of 909 people (451 males and 458 females) subjected to screening related analyses by the above-mentioned method were shown in Fig. 5. In males, no significant difference was found in age, BMI, and frequency of conventional risk factors of coronary artery disease such as smoking, hypertension, diabetes, hypercholesterolemia, hyperuricemia, etc. between myocardial infraction group and control group. In females, no significant difference was found in age, BMI, and frequency of hypercholesterolemia, hyperuricemia, etc. was not found between myocardial infraction group and control group, but the prevalence of smoking or diabetes was significantly higher in myocardial

infarction group as compared with the control group. In the screening-related analysis between 112 polymorphisms and myocardial infarction, by the multivariate logistic regression analysis in which age, BMI, and conventional risk factors for coronary artery disease such as smoking, hypertension, diabetes, hypercholesterolemia, hyperuricemia were corrected, 19 single nucleotide polymorphisms (SNP) in males and 18 single nucleotide polymorphisms (SNP) in females were shown to be associated with myocardial infarction (Fig. 6). Note here that in the screening-related analyses, category, in which P value < 0.1 in logistic regression analysis shows to have relation, was employed. In these SNPs, four SNPs were related to myocardial infarction in both males and females and other SNPs were related to myocardial infarction in either one of males or females.

Then, the determination of the genotype of these polymorphisms was carried out in the rest 4152 cases (male myocardial infarction subjects: 1784, male control: 1074, female myocardial infarction subjects: 590 and female control: 704). A large scale association study of these polymorphisms and myocardial infarction was carried out in total 5061 cases (male myocardial infarction subjects: 2003, male control: 1306, female myocardial infarction subjects: 816 and female control: 936).

Fig. 7 shows background data of the total 5061 cases (3309 males and 1752 females) in the large scale association study. In males, no significant difference was found in age, BMI and frequency of smoking between the myocardial infarction group and the control group, but the prevalence of hypertension or hyperuricemia was significantly lower in myocardial infarction group as compared

with the control group, and the prevalence of diabetes or hypercholesterolemia was significantly higher in myocardial infarction group as compared with the control group. In females, no significant difference in age or the prevalence of hypertension was found between the infarction group and the control group, but BMI and the prevalence of smoking, diabetes, hypercholesterolemia,or hyperuricemia was significantly higher in myocardial infarction group as compared with the control group. In a large scale association study of myocardial infarction in the males (19 SNP) and females (18 SNP), by the multivariable logistic regression analysis in which age, BMI, and frequency of smoking, hypertension, diabetes, hypercholesterolemia, hyperuricemia were corrected, 10 SNPs in males and 5 SNPs in females showed significant relation to the myocardial infarction ($P < 0.05$ in either of dominant or recessive gene model) (Fig. 8). Distribution of the genotypes and results of logistic regression analysis are shown in Figs. 8 and 9, respectively.

In this Example, a stepwise forward selection method of multivariate logistic regression analysis was carried out (see Fig. 10). This method employed dominant or recessive genetic model based on P value in relation to the myocardial infarction of the respective SNPs shown in Fig. 9. Fig. 10 shows gene locus on the chromosome of these genes. The -819T→C polymorphism and -592A→C polymorphism in the interleukin-10 were in linkage disequilibrium [pairwise linkage disequilibrium coefficient, D' (D/D_{max}), of 0.406; standardized linkage disequilibrium coefficient, r, of 0.396; $P < 0.0001$, chi-square test]. Gene loci of tumor necrosis factor α gene and platelet-activating factor acetylhydrolase gene were in proximity to each other, but no relationship was found

in distribution of the genotype of polymorphisms of the both genes. Similarly, gene loci of plasminogen activator inhibitor 1 gene and paraoxonase were in proximity to each other, but no relationship was found in distribution of the genotype of polymorphisms of the both genes.

The odds ratio of contraction with myocardial infarction by the combination of the genotype calculated by the stepwise forward selection method was shown in Fig. 11 and Fig. 13 (A) as to males, and in Fig. 12 and Fig. 13 (B) as to females. In males, maximum odds ratio was 4.50 in the genotype combination of five SNPs (TSP4 (1186G→C) polymorphism, connexin 37 (1019C→T) polymorphism, PAF acetylhydrolase (994G→T) polymorphism, angiotensinogen (-6G→A) polymorphism, tumor necrosis factor α (-863C→A) polymorphism) (see Fig. 11 and Fig. 13(A)). In the case where further five SNPs (SNP (NADH/NADPH oxidase p22 phox (242C→T) polymorphism, Apo E (-219G→T) polymorphism, Apo C-III (-482C→T) polymorphism, IL-10 (-819T→C) polymorphism, IL-10 (-592A→C) polymorphism) were added and SNPs are 10 in total, maximum odds ratio was 11.26 (see Fig. 10 and Fig. 13 (A)). In females, by the combination of five SNP (Apo E (4070C→T) polymorphism, glycoprotein Ibα (1018C→T) polymorphism, stromelysin 1 (-1171/5A→6A) polymorphism, PAI1 (-668/4G→5G) polymorphism, paraoxonase (584G→A) polymorphism)), maximum odds ratio was 88.51 (see Fig. 12 and Fig. 13(B)).

As mentioned above, the present inventors have investigated the relationship between myocardial infarction and 112 polymorphisms which were selected from 71 candidate genes; and identified 10 SNPs (in males) and five SNPs (in females) which

were associated with myocardial infarction by way of a large scale association study of 5061 cases. Furthermore, by the stepwise forward selection method of multivariate logistic regression analysis, a method for diagnosing the risk of myocardial infarction (genetic risk diagnostic system) presenting the maximum odds ratio of 11.26 in males and maximum odds ratio of 88.51 was developed.

Main causes of myocardial infarction is arteriosclerotic coronary artery disease, which may cause hemodynamically significant stenosis in the internal diameter of artery to cause abnormalities in regulation of vasoconstriction and vasodilator action. As a result, rupture of arterial sclerosis lesion or thrombogenesis is likely to occur. The present inventors have selected 71 candidate genes based on the comprehensive viewpoint including vascular biology, platelet-leukocyte biology, coagulation and fibrinolysis system, a metabolic factor such as lipid, sugar, etc. In fact, a group of genes related to myocardial infarction had various roles in development condition. That is to say, vascular biology (connexin 37, NADH/NADPH oxidase p22 phox, and thrombospondin 4), vascular inflammation (tumor necrosis factor-α, platelet-activating factor acetylhydrolase, and interleukin-10), hypertension (angiotensinogen), lipid metabolism (apolipoprotein E and C-III and paraoxonase), function of platelet (glycoprotein Iba), matrix metabolism (stromelysin-1), fibrinolytic system (PAI-1), and the like, are included (Boerma M, Forsberg L, van Zeijl L, et al. A genetic polymorphism in connexin 37 as a prognostic marker for atherosclerotic plaque development. J Intern Med 1999;246: 211-218, Inoue N, Kawashima S, Kanazawa K, Yamada S, Akita H, Yokoyama M. Polymorphism of the NADH/NADPH oxidase p22 phox gene in patients with coronary artery disease.

Circulation 1998;97: 135-137, Topol EJ, McCarthy J, Gabriel S, et al. Single nucleotide polymorphisms in multiple novel thrombospondin genes may be associated with familial premature myocardial infarction. Circulation 2001;104: 2641-2644, Skoog T, van't Hooft FM, Kallin B, et al. A common functional polymorphism (C→A substitution at position -863) in the promoter region of the tumor necrosis factor-α (TNF-α) gene associated with reduced circulating level of TNF-α. Hum Mol Genet 1999;8: 1443-1449, Yamada Y, Ichihara S, Fujimura T, Yokota M. Identification of the G^{994}→T missense mutation in exon 9 of the plasma platelet-activating factor acetylhydrolase gene as an independent risk factor for coronary artery disease in Japanese men. Metabolism 1998;47: 177-181, Koch W, Kastrati A, Bottiger C, Mehilli J, von Beckerath N, Schomig A. Interleukin-10 and tumor necrosis factor gene polymorphisms and risk of coronary artery disease and myocardial infarction. Atherosclerosis 2001;159: 137-144, Inoue I, Nakajima T, Williams CS, et al. A nucleotide substitution in the promoter of human angiotensinogen is associated with essential hypertension and affects basal transcription in vitro. J Clin Invest 1997;99: 1786-1797, Lambert J-C, Brousseau T, Defosse V, et al. Independent association of an APOE gene promoter polymorphism with increased risk of myocardial infarction and decreased APOE plasma concentrations-the ECTIM study. Hum Mol Genet 2000;9: 57-61, Eto M, Watanabe K, Makino I. Increased frequency of apolipoprotein epsilon 2 and epsilon 4 alleles in patients with ischemic heart disease. Clin Genet 1989;36: 183-188., Ruiz J, Blanche H, James RW, et al. Gln-Arg192 polymorphism of paraoxonase and coronary heart disease in type 2 diabetes. Lancet 1995;346: 869-72, Murata M, Matsubara Y, Kawano K, et al. Coronary artery disease and polymorphisms in a receptor mediating shear stress-dependent

platelet activation. Circulation 1997;96: 3281-3286, Eriksson P, Kallin B, van't Hooft FM, Bavenholm P, Hamsten A. Allele-specific increase in basal transcription of the plasminogen-activator inhibitor 1 gene is associated with myocardial infarction. Proc Natl Acad Sci USA 1995;92: 1851-1855, Ye S, Watts GF, Mandalia S, Humphries SE, Henney AM. Preliminary report: genetic variation in the human stromelysin promoter is associated with progression of coronary atyherosclerosis. Br Heart J 1995; 73: 209-215). The present inventors have investigated 112 gene polymorphisms in 909 cases and investigated 19 SNPs in 2858 male cases and 18 SNPs in 1294 female cases. As a result, the present inventors determined 179,402 genotypes in total. The number of determined genes is the largest among those reported previously in the last relation analysis of gene polymorphisms. The method for diagnosing the risk of myocardial infarction shown in the above-mentioned Examples had maximum odds ratio of 11.26 in males and 88.51 in females, which are also maximum among those in the previously reported relation analysis.

In 15 SNPs associated with myocardial infarction, 4070T→C (Arg158Cys) polymorphism of the apolipoprotein E gene exhibited a maximum odds ratio as female myocardial infarction. Apolipoprotein E is a main component of chylomicron and very low density lipoprotein (VLDL) remnant and functions as ligand when these lipoporoteins are taken by receptors in the liver (Mahley RW. Apolipoprotein E: cholesterol transport protein with expanding role in cell biology. Science 1998;240: 622-630). 158Cys (e2) allele of apolipoprotein E gene causes abnormal binding to the receptor in the liver (Schneider WJ, Kovanen PT, Brown MS, et al. Familial dysbetalipoproteinemia. Abnormal binding of mutant

apolipoprotein E to low density lipoprotein receptors of human fibroblasts and membranes from liver and adrenal of rats, rabbits, and cows. J Clin Invest 1981;68: 1075-1085), and the removal from plasma is delayed (Gregg RE, Zech LA, Schaefer EJ, Brewer HB Jr. Type III hyperlipoproteinemia: defective metabolism of an abnormal apolipoprotein E. Science 1981;211: 584-586). Most of familial dysbetalipoproteinemia (FD, or III type hyperlipoproteinemia) patients have homozygote of Arg158Cys polymorphism (Breslow JL, Zannis VI, SanGiacomo TR, Third JL, Tracy T, Glueck CJ. Studies of familial type III hyperlipoproteinemia using as a genetic marker the apo E phenotype E2/2. J Lipid Res 1982;23: 1224-1235). However, since only 1% to 4% of 158Cys/Cys homozygote develops familial dysbetalipoproteinemia, it is thought that other genetic factors or environmental factors are necessary to this disease. Accumulation of arteriosclerosis remnant lipoprotein (β-VLDL) in plasma in familial dysbetalipoproteinemia patients (Mahley RW. Apolipoprotein E: cholesterol transport protein with expanding role in cell biology. Science 1998;240: 622-630) or a mouse over-expressing human 158Cys/Cys (Sullivan PM, Mezdour H, Quarfordt SH, Maeda N. Type III hyperlipoproteinemia and spontaneous atherosclerosis in mice resulting from gene replacement of mouse Apoe with human APOE*2. J Clin Invest 1998;102: 130-135) is found to promote the development of arteriosclerosis. Eto et al. have reported that e2 (158Cys) allele is associated with coronary artery disease in Japanese males (odds ratio=2.44, e2 allele pair, e3/e3 type) and females (odds ratio=3.03) (Eto M, Watanabe K, Makino I. Increased frequency of apolipoprotein epsilon 2 and epsilon 4 alleles in patients with ischemic heart disease. Clin Genet 1989;36: 183-188). The conclusion of the present inventors that TT type (158Cys/Cys) is a risk factor for

myocardial infarction agrees with the conclusion of Eto et al.

Some of SNPs investigated in the above-mentioned Examples may be in a linkage disequilibrium with SNPs of genes actually associated with the development of myocardial infarction existing in the vicinity thereof. However, nine genes in male and five genes in females are shown to be susceptible gene loci of myocardial infarction. Furthermore, combination of genotypes enables high reliable and predictability diagnostic method. Thus, diagnostic method of the present invention can be expected to contribute to primary prevention of myocardial infarction and the improvement in quality of life of middle and old aged persons as well as the reduction of health care cost.

The present invention is not limited to the description of the above embodiments. A variety of modifications, which are within the scopes of the following claims and which are achieved easily by a person skilled in the art, are included in the present invention.

Hereinafter, the following matters are disclosed.

11. A method for detecting the genotype, comprising the following step (a1),

(a1) analyzing the following polymorphisms (1) to (10) in a nucleic acid sample:

(1) polymorphism at the base number position 1019 of the connexin 37 gene;

(2) polymorphism at the base number position -863 of the tumor necrosis factor α gene;

(3) polymorphism at the base number position 242 of the

NADH/NADPH oxidase p22 phox gene;

(4) polymorphism at the base number position -6 of the angiotensinogen gene;

(5) polymorphism at the base number position -219 of the apolipoprotein E gene;

(6) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(8) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(9) polymorphism at the base number position -819 of the interleukin-10 gene; and

(10) polymorphism at the base number position -592 of the interleukin-10 gene.

12. A method for detecting the genotype, comprising the following step (b1),

(b1) analyzing the following polymorphisms (11) to (15) in a nucleic acid sample:

(11) polymorphism at the base number position -1171 of the stromelysin 1 gene;

(12) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) polymorphism at the base number position 1018 of the glycoprotein Ibα gene;

(14) polymorphism at the base number position 584 of the paraoxonase gene: and

(15) polymorphism at the base number position 4070 of the apolipoprotein E gene.

13. A method for diagnosing the risk of myocardial infarction, comprising the following (i) to (iii):

(i) a step of analyzing the following polymorphisms (1) to (10) in a nucleic acid sample:

(1) polymorphism at the base number position 1019 of the connexin 37 gene;

(2) polymorphism at the base number position -863 of the tumor necrosis factor α gene;

(3) polymorphism at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) polymorphism at the base number position -6 of the angiotensinogen gene:

(5) polymorphism at the base number position -219 of the apolipoprotein E gene;

(6) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(8) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(9) polymorphism at the base number position -819 of the interleukin-10 gene; and

(10) polymorphism at the base number position -592 of the interleukin-10 gene;

(ii) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(iii) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

14. A method for diagnosing the risk of myocardial infarction, comprising the following steps (iv) to (vi):

(iv) a step of analyzing the following polymorphisms (11) to (15) in a nucleic acid sample:

(11) polymorphism at the base number position -1171 of the stromelysin 1 gene;

(12) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) polymorphism at the base number position 1018 of the glycoprotein Ibα gene;

(14) polymorphism at the base number position 584 of the paraoxonase gene: and

(15) polymorphism at the base number position 4070 of the apolipoprotein E gene.

(v) determining, based on the information about polymorphism which was obtained in the step (iv), the genotype of the nucleic acid sample; and

(vi) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

INDUSTRIAL APPLICABILITY

According to the present invention, gene polymorphisms associated with myocardial infarction are analyzed and the genotypes of nucleic acid sample are detected. By using the information about polymorphisms obtained by the detection of the genotypes, diagnosis of the risk of myocardial infarction with high accuracy and high predictability can be carried out. Therefore, the present invention is an effective means for understanding the risk of development of myocardial infarction

in advance. Furthermore, according to the present invention, auxiliary information useful for diagnosing the disease is obtained, thus enabling more appropriate treatment and improvement of prognosis. In addition, the present invention provides information useful in clarifying the development mechanism of myocardial infarction and is expected to contribute to prevention and treatment of myocardial infarction.